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PATENT

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In re Application of:
R. Sanders Williams and
Beverly Rothermel

Serial No.: Unknown

Filed: February 13, 2001

For: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE CALCINEURIN INTERACTING PROTEIN (MCIP)

Group Art Unit: Unknown

Examiner: Unknown

Atty. Dkt. No.: UTSD:674US

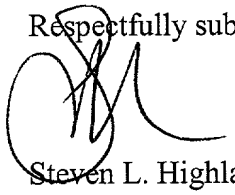
STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(f)

BOX SEQUENCE
Commissioner for Patents
Washington, D.C. 20231

Commissioner:

Submitted herewith is a computer readable form and a paper copy of the sequence listing of those sequences in the captioned patent application. The computer readable form of the sequence listing is the same as the paper copy of the sequence listing. The sequence information provided in the Specification is also the same as the sequence listing of the enclosed computer readable and paper forms of the sequence listing.

Respectfully submitted,



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Reg. No. 37,642
Attorney for Applicants

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Austin, Texas 78701
(512) 536-3184

Date: February 13, 2001

SEQUENCE LISTING

<110> WILLIAMS, R. SANDERS
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Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
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Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Glu Met Glu Arg
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Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
             20                  25                  30

gag gga ctg ttc cgg acc tat gat gaa tgt gtg acg ttc cag ctg ttt     144
Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
         35                  40                  45

aag agt ttc cga cgg gtt cga ata aat ttc agc cat ccc aaa tct gca     192
Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
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Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
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Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
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Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
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Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
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1 5 10 15

Val Ala Asn Ser Asp Ile Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe

20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 14
<211> 2212
<212> DNA
<213> Homo sapiens

<220>
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<222> (25)..(615)

<400> 14
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Met Glu Glu Val Asp Leu Gln Asp Leu
1 5

ccc agc gcc acc atc gcc tgt cac ctg gac ccg cgc gtg ttc gtg gac 99
Pro Ser Ala Thr Ile Ala Cys His Leu Asp Pro Arg Val Phe Val Asp
10 15 20 25

ggc ctg tgc cgg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag 147
Gly Leu Cys Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys
30 35 40

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gac atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac   195
Asp Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn
            45                  50                  55

ttc agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag   243
Phe Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys
        60                  65                  70

act gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta   291
Thr Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu
    75                  80                  85

cac ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt   339
His Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe
90                  95                  100                 105

ctg atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa   387
Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu
                110                 115                 120

gat gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag   435
Asp Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys
            125                 130                 135

ctg ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act   483
Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr
        140                 145                 150

ccc agc gtg gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa   531
Pro Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu
    155                 160                 165

gaa gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag   579
Glu Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln
170                 175                 180                 185

acc agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca        625
Thr Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser
                190                 195

cgcgacgagg acgcattcca aatcatactc acgggaggaa tcttttactg tggaggtggc 685

tggtcacgac ttcttcggag gtggcagccg agatcggggt ggcagaaatc ccagttcatg 745

ttgctcagaa gagaatcaag gccgtgtccc cttgttctaa tgctgcacac cagttactgt 805

tcatggcacc cgggaatgac ttgggccaat cactgagttt gtggtgatcg cacaaggaca 865

tttgggactg tcttgagaaa acagataatg atagtgtttt gtacttgttc ttttctggta 925

ggttctgtct gtgccaaggg caggttgatc agtgagctca ggagagagct tcctgtttct 985

aagtggcctg caggggccac tctctactgg taggaagagg taccacagga agccgcctag 1045

tgcagagagg ttgtgaaaac agcagcaatg caatgtggaa attgtagcgt ttcctttctt 1105
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ccctcatgtt ctcatgtttg tgcatgtata ttactgattt acaagactaa cctttgttcg 1165

tatataaagt tacaccgttg ttgttttaca tcttttggga agccaggaaa gcgtttggaa 1225

aacgtatcac ctttcccaga ttctcggatt ctcgactctt tgcaacagca cttgcttgcg 1285

gaactcttcc tggaatgcat tcactcagca tccccaaccg tgcaacgtgt aacttgtgct 1345

tttgcaaaag aagttgatct gaaattcctc tgtagaattt agcttataca attcagagaa 1405

tagcagtttc actgccaact tttagtgggt gagaaatttt agtttaggtg tttgggatcg 1465

gacctcagtt tctgttgttt cttttatgtg gtggtttcta tacatgaatc atagccaaaa 1525

actttttgg aaactgttgg ttgagatagt tggttctttt accccacgaa gacatcaaga 1585

tacacttgta aataaagctg atagcatata ttcatacctg ttgtacactt gggtgaaaag 1645

tatggcagtg ggagactaag atgtattaac ctacctgtga atcatatgtt gtaggaaaag 1705

ctgttcccat gtctaacagg acttgaattc aaagcatgtc aagtggatag tagatctgtg 1765

gcgatatgag agggatgcag tgcctttccc cattcattcc tgatggaatt gttatactag 1825

gttaacattt gtaatttttt tctagttgta atgtgtatgt ctggtaaata ggtattatat 1885

tttggcctta caataccgta acaatgtttg tcattttgaa atacttaatg ccaagtaaca 1945

atgcatgctt tggaaatttg gaagatggtt ttattctttg agaagcaaat atgtttgcat 2005

taaatgcttt gattgttcat atcaagaaat tgattgaacg ttctcaaacc ctgtttacgg 2065

tacttggtaa gagggagccg gtttgggaga gaccattgca tcgctgtcca agtgtttctt 2125

gttaagtgct tttaaactgg agaggctaac ctcaaaatac ttttttttaac tgcattctat 2185

aataaatggg cacagtatgc tccttac 2212

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<211> 197
<212> PRT
<213> Homo sapiens

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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 16
<211> 197
<212> PRT
<213> Homo sapiens

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Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
1 5 10 15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 17
<211> 3184
<212> DNA
<213> Homo sapiens

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<222> (205)..(780)

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cgagcctcca gccgtcctca gagcaaggca gcaccgaggc ctggccacag caatatccat 120

ctggaagctc ttcccttcac tcccaactct gaggttgcct aactctttat taaaaattca 180

gaagggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231
Met Asp Cys Asp Val Ser Thr Leu Val
1 5

gcc tgt gtg gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279
Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu
10 15 20 25

aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327
Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln
30 35 40

cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375
Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys
45 50 55

tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg 423
Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly
60 65 70

aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat 471
Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp
75 80 85

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gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc   519
Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu
 90                  95                  100                 105

atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat   567
Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp
                110                 115                 120

gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta   615
Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu
            125                 130                 135

gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca   663
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro
        140                 145                 150

agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gaa gag gac   711
Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp
    155                 160                 165

cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc   759
Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly
170                 175                 180                 185

ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatagcc      810
Leu Pro Pro Ser Val Ser Asn
                190

gtctcctctt tatcatgctt tttccccctg ttgtttgtca aaaaaaattg cctttaaatt 870

cctgggtgtt tggttgtttg agattccttc cttgttatca agcctctcgg acaaaagggc 930

taggaaaagg tgatatgtct cctgatcata tcatacccat taagtataac ccattattta 990

gaaggttcta gggaaaaaag tagtattttc ttattaaaca atcagcacag cctatatctt 1050

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agatttcaaa caccactccc ctgtagaact ctcccagcct cgttggggag gcttgtccag 1530

ggtgatagag actgatttca gacaaaccta tttattacaa aagtttcatg gtgtctgaat 1590

gattgttttc tctctttgta tatttgtaca aatgtttcag ctgtgctttt aaaaaatctg 1650
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gatgtttttt atttagtgat tgttcgacaa ttagctgctt caaaacataa tgtgcattgc 1710

ttatgaatgc cttcatatac taatacagat actctgataa tattacactc taataaggat 1770

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gtttttgtta cgtgtgattt tcctatttct ctagcccaaa gtgcattaca gaagatacac 2070

ctatagaacc attaccttct gctatgtgtg ccagggctca tctactcctg tacattaatg 2130

gattacttta gatgcaaatg cagattacaa tggagtgggg aagtactttc attacccaag 2190

cctcagaaaa acacacaaga acaataacac agcaaacaga ttgagggatt gttgtggttt 2250

ttgactaagg tgtatgttag tttcatcaga aacttaaaac atagactgat cactcagaaa 2310

ttaaagtccg ttttactgtg aatatagcaa tatagtactg gacacagtac tggtgaaact 2370

gaggagagca ttgcttgtaa aatcctgagt ttccataagg aaaatgaaaa ctccttttaa 2430

aaataaaatc tgaggagtgt acaataagca tatgctttga ctttcctttg ctgtggaggt 2490

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tagtggaaga aatagtagct ccgctattca gatgcagagc actgcagcat ccagcctttc 2610

aaagctgact cttctcaatc atctgtgggt catttgactt gatttttttaa gctaccctga 2670

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taaatgtttt ttaaaagaca catctgacat ttttaacaac ttagtaaaag ttgaaatgac 2790

cattctgtgt agtcataaaa gaaacacaat gaagtgtatg gcctctggag ttagtcttag 2850

taaaacttat tgctctgtgt caatgttaac ctgtctcaga tcaagtaatt ccttcactag 2910

gttgggtttg gggagggggg aaaagagggg cttttcctag gagaacgata agaaatggaa 2970

agactccttg aagtgttgca agggaacctc ctagcactgt gaaagtcaga atcgcctcag 3030

catttccatg acgcacatta tgcaaatctc tttagcacta ttttaaggtt gaaaacttta 3090

acaatgaagg ggaaggggaa gatttccacc aactgaatca tttgtgcacg tgtatagctc 3150

aaagagctta gacttcaaat atatctggtg aatg 3184

<210> 18
<211> 192
<212> PRT
<213> Homo sapiens

<400> 18
Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 19
<211> 192
<212> PRT
<213> Homo sapiens

<400> 19
Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 20
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (23)..(745)

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Met Leu Arg Asp Thr Met Lys Ser Trp Asn
1 5 10

gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gaa gag 100
Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu
15 20 25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta 148
Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
30 35 40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg 196
Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
45 50 55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc 244
Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile

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     60                  65                  70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc   292
Tyr Asp Asp Gln Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg Val
 75                  80                  85                  90

aga ata aat ttc agc aaa cct gaa gcg gca gca aga gcg cga ata gaa   340
Arg Ile Asn Phe Ser Lys Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu
                 95                 100                 105

ctc cac gaa aca gac ttc aat ggg cag aag cta aag cta tat ttt gca   388
Leu His Glu Thr Asp Phe Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala
            110                 115                 120

cag gtg cag atg tcc ggc gaa gtg cgg gac aag tcc tat ctc ctg ccg   436
Gln Val Gln Met Ser Gly Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro
        125                 130                 135

ccc cag cct gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca   484
Pro Gln Pro Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro
    140                 145                 150

gtg ggg tgg aag cag agc gaa gat gcg atg cct gtt ata aat tat gat   532
Val Gly Trp Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp
155                 160                 165                 170

tta ctc tgt gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt   580
Leu Leu Cys Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu
                175                 180                 185

cac gcg gga aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa   628
His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu
            190                 195                 200

agt gaa act gaa gag gaa gaa gag aca aaa aac ccc aaa cag aaa att   676
Ser Glu Thr Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile
        205                 210                 215

gcc cag aca agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc   724
Ala Gln Thr Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro
    220                 225                 230

cag acc ttt gat tgc gcg ctg tgaggccctt ggttgtggtg cgaggcggct      775
Gln Thr Phe Asp Cys Ala Leu
235                 240

gccctggtgg gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg        828


<210> 21
<211> 241
<212> PRT
<213> Homo sapiens

<400> 21
Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
  1               5                  10                  15
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Cys Ser Thr Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 22
<211> 241
<212> PRT
<213> Homo sapiens

<400> 22
Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
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Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
20 25 30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
35 40 45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
50 55 60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65 70 75 80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
85 90 95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
100 105 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
115 120 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
130 135 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145 150 155 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
165 170 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 23
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(637)

<400> 23
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    1               5                  10                  15

ttg gat gag atg atg gat tta agt gat ctg cct acc tca ctt ttt gct   97
Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
            20                  25                  30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga   145
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
        35                  40                  45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg   193
Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
    50                  55                  60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg   241
Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65                  70                  75                  80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag   289
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
                85                  90                  95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct   337
Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
            100                 105                 110

gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg   385
Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
        115                 120                 125

aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt   433
Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
    130                 135                 140

gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga   481
Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145                 150                 155                 160

aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act   529
Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
                165                 170                 175

gaa gag gaa gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca   577
Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
            180                 185                 190

agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt   625
Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
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gat tgc gcg ctg tgaggccctt ggttgtggtg cgaggcggct gccctggtgg       677
Asp Cys Ala Leu
    210

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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
             20                  25                  30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
         35                  40                  45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
     50                  55                  60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
 65                  70                  75                  80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
                 85                  90                  95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
            100                 105                 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
        115                 120                 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
    130                 135                 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145                 150                 155                 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
                165                 170                 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
            180                 185                 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
        195                 200                 205

Asp Cys Ala Leu
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Asp Gln Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
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Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
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<212> DNA
<213> Homo sapiens

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aattaacttt gcttggggag aatggaaaaa acagctgagg tttgcttcac agctgcttta 420
tcaacctctc ttgcagcata gtttccactg gtagtaattc cattcagcta ctcagacaac 480

acgctcctcg gccgaatggg acgacccttc ttaagatgga aaatgttaca aaagaaaaag 540
gatgaaggtc tgtggcaata aacagcaatt agactgtagg gaaatttcaa ggctttggga 600
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ccatttatgc cagaggttg 1039

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atgaaaatcc taggattgtt ttaggttctg tttgctccat tccactgtgg gatacaagta 180
gaaattggga cattcatcca ataaaatgtc actggggaaa aaaattttaa ctacacttca 240
aaatgattcc tctttttgtc ctttaaaatt tttattgacc aagacagatt tcaaaatgtt 300
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cacctctttc cagtagaaac ttacactttg tccctgtcta cctgcaagca tgcaggactt 720
gactcaggaa tttgctgtcc aaacaggatg ctgtggaagc tgcacttttt ttttccccag 780
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SEQUENCE LISTING

<110> WILLIAMS, R. SANDERS
ROTHERMEL, BEVERLY

<120> METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE CALCINEURIN INTERACTING PROTEIN (MCIP)

<130> UTSD:674US

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<141> 2001-02-13

<150> 60/216,601
<151> 2000-07-07

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gttggctgga aacaagtaga agatgccacc cccgtcataa attacgatct tttatatgcc 480
atctccaagc tggggccagg agagaagtat gaactgcatg cagcgacaga caccactccc 540
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<222> (1)..(594)

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 1               5                  10                  15

cac ctg gac ccg cgc gtg ttc gtg gac ggc ctg tgc cgg gcc aaa ttt   96
His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
            20                  25                  30

gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt   144
Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
        35                  40                  45

aag agc ttc aaa cgt gtc cgg ata aac ttc agc aac ccc tta tct gca   192
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
    50                  55                  60

gcc gat gcc agg ctg cgg ctg cac aag acc gag ttc ctg ggg aag gaa   240
Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65                  70                  75                  80

atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg   288
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                85                  90                  95

gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct   336
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat   384
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat   432
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140

gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtg gtc cac gtg   480
Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga   528
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
                165                 170                 175

atg aag aga ccc aag ccc aaa atc atc cag aca cgg aga ccg gag tac   576
Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
            180                 185                 190
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aca ccg atc cac ctt agc tga 597
Thr Pro Ile His Leu Ser
195

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20 25 30

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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser

195

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Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
 1               5                  10                  15

His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
            20                  25                  30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
        35                  40                  45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
    50                  55                  60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65                  70                  75                  80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                85                  90                  95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Glu Met Glu Arg
                165                 170                 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
            180                 185                 190

Thr Pro Ile His Leu Ser
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  1               5                  10                  15

gtg gca aac gat gat gtc ttc agc gaa agt gag acc agg gcc aaa ttt   96
Val Ala Asn Asp Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
             20                  25                  30

gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt   144
Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
         35                  40                  45

aag agc ttc aaa cgt gtc cgg ata aac ttc agc aac ccc tta tct gca   192
Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
     50                  55                  60

gcc gat gcc agg ctg cgg ctg cac aag acc gag ttc ctg ggg aag gaa   240
Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65                  70                  75                  80

atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg   288
Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                 85                  90                  95

gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct   336
Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat   384
Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat   432
Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140
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gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtg gtc cac gtg   480
Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga   528
Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
                165                 170                 175

atg aag aga ccc aag ccc aaa atc atc cag aca cgg aga ccg gag tac   576
Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
            180                 185                 190

aca ccg atc cac ctt agc tga                                      597
Thr Pro Ile His Leu Ser
        195
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Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
         35                  40                  45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
     50                  55                  60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65                  70                  75                  80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                 85                  90                  95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
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130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser
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35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
50 55 60

Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
165 170 175

Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
180 185 190

Thr Pro Ile His Leu Ser
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Met Pro Ala Pro Ser Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys
  1               5                  10                  15

gtg gtg gat gtg gag gtc ttt acc aat cag gag gtt aag gaa aaa ttc   96
Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
             20                  25                  30

gag gga ctg ttc cgg acc tat gat gaa tgt gtg acg ttc cag ctg ttt  144
Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
         35                  40                  45

aag agt ttc cga cgg gtt cga ata aat ttc agc cat ccc aaa tct gca  192
Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
     50                  55                  60

gcc cgt gcc cgg ata gag ctt cat gag act cag ttc aga ggg aag aag  240
Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
 65                  70                  75                  80

cta aaa ctc tac ttc gcc cag gtc cag acc cca gag aca gat gga gac  288
Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
                 85                  90                  95
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aaa ctg cat ttg gca cct cca cag cct gcc aaa cag ttc ctc atc tca   336
Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
            100                 105                 110

ccc cct tca tct cct cct gtt ggc tgg aag cct atc agc gat gcc aca   384
Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
        115                 120                 125

cca gtc ctc aac tat gac ctt ctt tat gct gtg gcc aaa cta gga cca   432
Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
    130                 135                 140

gga gag aaa tat gag ctg cac gct gga act gag tct aca ccg agc gtc   480
Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145                 150                 155                 160

gtg gtg cat gtg tgt gac agc gac atg gag gag gag gag gac cca aag   528
Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Glu Asp Pro Lys
                165                 170                 175

act tcc ccc aag cca aaa atc att cag acc cgg cgt ccg ggc ttg cca   576
Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
            180                 185                 190

ccc tcc gtg tcc aac tga                                          594
Pro Ser Val Ser Asn
        195
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             20                  25                  30

Glu Gly Leu Phe Arg Thr Tyr Asp Glu Cys Val Thr Phe Gln Leu Phe
         35                  40                  45

Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
     50                  55                  60

Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
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Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
130 135 140

Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Glu Asp Pro Lys
165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
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Pro Ser Val Ser Asn
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35 40 45

Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser His Pro Lys Ser Ala
50 55 60

Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
65 70 75 80

Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
100 105 110

Pro Pro Ser Ser Pro Pro Val Gly Trp Lys Pro Ile Ser Asp Ala Thr
115 120 125

Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
130 135 140

Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
145 150 155 160

Val Val His Val Cys Asp Ser Asp Met Glu Glu Glu Glu Asp Pro Lys
165 170 175

Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
180 185 190

Pro Ser Val Ser Asn
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<213> Homo sapiens

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cgctttcact gtaagaaagc aag atg cat ttt aga aac ttt aac tac agt ttt 173
Met His Phe Arg Asn Phe Asn Tyr Ser Phe
1 5 10

agc tcc ctg att gcc tgt gtg gca aac agt gat atc ttc agc gaa agt 221
Ser Ser Leu Ile Ala Cys Val Ala Asn Ser Asp Ile Phe Ser Glu Ser
15 20 25

gaa acc agg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag gac 269
Glu Thr Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp
30 35 40

atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac ttc 317
Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn Phe
45 50 55

agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag act 365
Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys Thr
60 65 70

gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta cac 413
Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu His
75 80 85 90

ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt ctg 461
Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu
95 100 105

atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa gat 509
Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu Asp
110 115 120

gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag ctg 557
Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu
125 130 135

ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act ccc 605
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr Pro
140 145 150

agc gtg gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa gaa 653
Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu
155 160 165 170

gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag acc 701
Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr
175 180 185

agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca cgcgacgagg 754
Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser
190 195

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gagaatcaag gccgtgtccc cttgttctaa tgctgcacac cagttactgt tcatggcacc 934

cgggaatgac ttgggccaat cactgagttt gtggtgatcg cacaaggaca tttgggactg 994

tcttgagaaa acagataatg atagtgtttt gtacttgttc ttttctggta ggttctgtct 1054

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<212> PRT
<213> Homo sapiens

<400> 12

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Val Ala Asn Ser Asp Ile Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
             20                  25                  30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
         35                  40                  45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
     50                  55                  60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
 65                  70                  75                  80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                 85                  90                  95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
                165                 170                 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
            180                 185                 190

Pro Ile His Leu Ser
        195
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<210> 13
<211> 197
<212> PRT
<213> Homo sapiens

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Met His Phe Arg Asn Phe Asn Tyr Ser Phe Ser Ser Leu Ile Ala Cys
 1               5                  10                  15

Val Ala Asn Ser Asp Ile Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
            20                  25                  30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
        35                  40                  45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
    50                  55                  60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65                  70                  75                  80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
                85                  90                  95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
            100                 105                 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
        115                 120                 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
                165                 170                 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
            180                 185                 190

Pro Ile His Leu Ser
        195
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ccc agc gcc acc atc gcc tgt cac ctg gac ccg cgc gtg ttc gtg gac 99
Pro Ser Ala Thr Ile Ala Cys His Leu Asp Pro Arg Val Phe Val Asp
10 15 20 25

ggc ctg tgc cgg gcc aaa ttt gag tcc ctc ttt agg acg tat gac aag 147
Gly Leu Cys Arg Ala Lys Phe Glu Ser Leu Phe Arg Thr Tyr Asp Lys
30 35 40

gac atc acc ttt cag tat ttt aag agc ttc aaa cga gtc aga ata aac 195
Asp Ile Thr Phe Gln Tyr Phe Lys Ser Phe Lys Arg Val Arg Ile Asn
45 50 55

ttc agc aac ccc ttc tcc gca gca gat gcc agg ctc cag ctg cat aag 243
Phe Ser Asn Pro Phe Ser Ala Ala Asp Ala Arg Leu Gln Leu His Lys
60 65 70

act gag ttt ctg gga aag gaa atg aag tta tat ttt gct cag acc tta 291
Thr Glu Phe Leu Gly Lys Glu Met Lys Leu Tyr Phe Ala Gln Thr Leu
75 80 85

cac ata gga agc tca cac ctg gct ccg cca aat cca gac aag cag ttt 339
His Ile Gly Ser Ser His Leu Ala Pro Pro Asn Pro Asp Lys Gln Phe
90 95 100 105

ctg atc tcc cct ccc gcc tct ccg cca gtg gga tgg aaa caa gtg gaa 387
Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Val Glu
110 115 120

gat gcg acc cca gtc ata aac tat gat ctc tta tat gcc atc tcc aag 435
Asp Ala Thr Pro Val Ile Asn Tyr Asp Leu Leu Tyr Ala Ile Ser Lys
125 130 135

ctg ggg cca ggg gaa aag tat gaa ttg cac gca gcg act gac acc act 483
Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Ala Thr Asp Thr Thr

140 145 150

ccc agc gtg gtg gtc cat gta tgt gag agt gat caa gag aag gag gaa 531
Pro Ser Val Val Val His Val Cys Glu Ser Asp Gln Glu Lys Glu Glu
155 160 165

gaa gag gaa atg gaa aga atg agg aga cct aag cca aaa att atc cag 579
Glu Glu Glu Met Glu Arg Met Arg Arg Pro Lys Pro Lys Ile Ile Gln
170 175 180 185

acc agg agg ccg gag tac acg ccg atc cac ctc agc tgaactggca 625
Thr Arg Arg Pro Glu Tyr Thr Pro Ile His Leu Ser
190 195

cgcgacgagg acgcattcca aatcatactc acgggaggaa tcttttactg tggaggtggc 685

tggtcacgac ttcttcggag gtggcagccg agatcggggt ggcagaaatc ccagttcatg 745

ttgctcagaa gagaatcaag gccgtgtccc cttgttctaa tgctgcacac cagttactgt 805

tcatggcacc cgggaatgac ttgggccaat cactgagttt gtggtgatcg cacaaggaca 865

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atgcatgctt tggaaatttg gaagatggtt ttattctttg agaagcaaat atgtttgcat 2005

taaatgcttt gattgttcat atcaagaaat tgattgaacg ttctcaaacc ctgtttacgg 2065

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aataaatggg cacagtatgc tccttac 2212

<210> 15
<211> 197
<212> PRT
<213> Homo sapiens

<400> 15

Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
115 120 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
130 135 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145 150 155 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
165 170 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
180 185 190

Pro Ile His Leu Ser
195

<210> 16
<211> 197
<212> PRT
<213> Homo sapiens

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Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
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His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
20 25 30

Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Ile Thr Phe Gln Tyr Phe
35 40 45

Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Phe Ser Ala
50 55 60

Ala Asp Ala Arg Leu Gln Leu His Lys Thr Glu Phe Leu Gly Lys Glu
65 70 75 80

Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
85 90 95

Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
100 105 110

Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn

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        115                 120                 125

Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
    130                 135                 140

Glu Leu His Ala Ala Thr Asp Thr Thr Pro Ser Val Val Val His Val
145                 150                 155                 160

Cys Glu Ser Asp Gln Glu Lys Glu Glu Glu Glu Glu Met Glu Arg Met
                165                 170                 175

Arg Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr Thr
            180                 185                 190

Pro Ile His Leu Ser
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ctggaagctc ttcccttcac tcccaactct gaggttgcct aactctttat taaaaattca 180

gaaggggggaa tgccagcccc tagc atg gac tgt gat gtt tcc act ctg gtt 231
                          Met Asp Cys Asp Val Ser Thr Leu Val
                            1   5

gcc tgt gtg gtg gat gtc gag gtc ttt acc aat cag gag gtt aag gaa 279
Ala Cys Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu
 10   15   20   25

aaa ttt ggg gga ctg ttt cgg act tat gat gac tgt gtg acg ttc cag 327
Lys Phe Gly Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln
                30   35   40

cta ttt aag agt ttc aga cgt gtc cgt ata aac ttc agc aat cct aaa 375
Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys

45 50 55

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tct gca gcc cga gct agg ata gag ctt cat gaa acc caa ttc aga ggg   423
Ser Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly
         60                  65                  70

aaa aaa tta aag ctc tac ttt gca cag gtt cag act cca gag aca gat   471
Lys Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp
     75                  80                  85

gga gac aaa ctg cac ttg gct cca ccc cag cct gcc aaa cag ttt ctc   519
Gly Asp Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu
 90                  95                 100                 105

atc tcg ccc cct tcc tcc cca cct gtt agc tgg cag ccc atc aac gat   567
Ile Ser Pro Pro Ser Ser Pro Pro Val Ser Trp Gln Pro Ile Asn Asp
                110                 115                 120

gcc acg cca gtc ctc aac tat gac ctc ctc tat gct gtg gcc aaa cta   615
Ala Thr Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu
            125                 130                 135

gga cca gga gag aag tat gag ctc cat gca ggg act gag tcc acc cca   663
Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro
        140                 145                 150

agt gtc gtc gtg cac gtg tgc gac agt gac ata gag gaa gaa gag gac   711
Ser Val Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp
    155                 160                 165

cca aag act tcc cca aag cca aaa atc atc caa act cgg cgt cct ggc   759
Pro Lys Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly
170                 175                 180                 185

ctg cca ccc tcc gtg tcc aac tgagctgcct gctccttctc gataatagcc      810
Leu Pro Pro Ser Val Ser Asn
                190
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gtctcctctt tatcatgctt tttccccctg ttgtttgtca aaaaaaattg cctttaaatt 870

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taaatgtttt ttaaaagaca catctgacat ttttaacaac ttagtaaaag ttgaaatgac 2790

cattctgtgt agtcataaaa gaaacacaat gaagtgtatg gcctctggag ttagtcttag 2850

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gttgggtttg gggaggggg aaaagagggg cttttcctag gagaacgata agaaatggaa 2970

agactccttg aagtgttgca agggaacctc ctagcactgt gaaagtcaga atcgcctcag 3030

catttccatg acgcacatta tgcaaatctc tttagcacta ttttaaggtt gaaaacttta 3090

acaatgaagg ggaaggggaa gatttccacc aactgaatca tttgtgcacg tgtatagctc 3150

aaagagctta gacttcaaat atatctggtg aatg 3184

<210> 18
<211> 192
<212> PRT
<213> Homo sapiens

<400> 18
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Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro

100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
130 135 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145 150 155 160

Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
165 170 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
180 185 190

<210> 19
<211> 192
<212> PRT
<213> Homo sapiens

<400> 19
Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys Val Val Asp Val Glu
1 5 10 15

Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe Gly Gly Leu Phe Arg
20 25 30

Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg
35 40 45

Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala Ala Arg Ala Arg Ile
50 55 60

Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys Leu Lys Leu Tyr Phe
65 70 75 80

Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp Lys Leu His Leu Ala
85 90 95

Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser Pro Pro Ser Ser Pro
100 105 110

Pro Val Ser Trp Gln Pro Ile Asn Asp Ala Thr Pro Val Leu Asn Tyr
115 120 125

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Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro Gly Glu Lys Tyr Glu
    130                 135                 140

Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys
145                 150                 155                 160

Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys Thr Ser Pro Lys Pro
                165                 170                 175

Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro Pro Ser Val Ser Asn
            180                 185                 190
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<210> 20
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (23)..(745)

<400> 20

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aaaaggccca ctttgggggga ta atg ctg agg gac act atg aaa tct tgg aat  52
                          Met Leu Arg Asp Thr Met Lys Ser Trp Asn
                            1               5                  10

gat agc cag tca gat ctg tgt agc act gac caa gaa gag gaa gaa gag   100
Asp Ser Gln Ser Asp Leu Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu
                15                  20                  25

atg att ttt ggt gaa aat gaa gat gat ttg gat gag atg atg gat tta   148
Met Ile Phe Gly Glu Asn Glu Asp Asp Leu Asp Glu Met Met Asp Leu
            30                  35                  40

agt gat ctg cct acc tca ctt ttt gct tgc agc gtc cat gaa gca gtg   196
Ser Asp Leu Pro Thr Ser Leu Phe Ala Cys Ser Val His Glu Ala Val
        45                  50                  55

ttt gag gca cga gag cag aag gaa aga ttt gaa gca ctc ttc acc atc   244
Phe Glu Ala Arg Glu Gln Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile
    60                  65                  70

tat gat gac cag gtt act ttt cag ctg ttt aaa agc ttt aga aga gtc   292
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Tyr Asp Asp Gln Val Thr Phe Gln Leu Phe Lys Ser Phe Arg Arg Val
75 80 85 90

aga ata aat ttc agc aaa cct gaa gcg gca gca aga gcg cga ata gaa 340
Arg Ile Asn Phe Ser Lys Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu
95 100 105

ctc cac gaa aca gac ttc aat ggg cag aag cta aag cta tat ttt gca 388
Leu His Glu Thr Asp Phe Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala
110 115 120

cag gtg cag atg tcc ggc gaa gtg cgg gac aag tcc tat ctc ctg ccg 436
Gln Val Gln Met Ser Gly Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro
125 130 135

ccc cag cct gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca 484
Pro Gln Pro Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro
140 145 150

gtg ggg tgg aag cag agc gaa gat gcg atg cct gtt ata aat tat gat 532
Val Gly Trp Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp
155 160 165 170

tta ctc tgt gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt 580
Leu Leu Cys Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu
175 180 185

cac gcg gga aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa 628
His Ala Gly Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu
190 195 200

agt gaa act gaa gag gaa gaa gag aca aaa aac ccc aaa cag aaa att 676
Ser Glu Thr Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile
205 210 215

gcc cag aca agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc 724
Ala Gln Thr Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro
220 225 230

cag acc ttt gat tgc gcg ctg tgaggccctt ggttgtggtg cgaggcggct 775
Gln Thr Phe Asp Cys Ala Leu
235 240

gccctggtgg gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg 828

<210> 21
<211> 241

<212> PRT
<213> Homo sapiens

<400> 21

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Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
  1               5                  10                  15

Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
             20                  25                  30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
         35                  40                  45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
     50                  55                  60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
 65                  70                  75                  80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
                 85                  90                  95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
            100                 105                 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
        115                 120                 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
    130                 135                 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145                 150                 155                 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
                165                 170                 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
            180                 185                 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
        195                 200                 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
    210                 215                 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225                 230                 235                 240
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Leu

<210> 22
<211> 241
<212> PRT
<213> Homo sapiens

<400> 22

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Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
 1               5                  10                  15

Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
            20                  25                  30

Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
        35                  40                  45

Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
    50                  55                  60

Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
65                  70                  75                  80

Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
                85                  90                  95

Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
            100                 105                 110

Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
        115                 120                 125

Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
    130                 135                 140

Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
145                 150                 155                 160

Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
                165                 170                 175

Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
            180                 185                 190
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Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 23
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(637)

<400> 23
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Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
1 5 10 15

ttg gat gag atg atg gat tta agt gat ctg cct acc tca ctt ttt gct 97
Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

tgc agc gtc cat gaa gca gtg ttt gag gca cga gag cag aag gaa aga 145
Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

ttt gaa gca ctc ttc acc atc tat gat gac cag gtt act ttt cag ctg 193
Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

ttt aaa agc ttt aga aga gtc aga ata aat ttc agc aaa cct gaa gcg 241
Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

gca gca aga gcg cga ata gaa ctc cac gaa aca gac ttc aat ggg cag 289
Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

aag cta aag cta tat ttt gca cag tcc tat ctc ctg ccg ccc cag cct 337

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Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
            100                 105                 110

gtc aag cag ttc ctc atc tcc cct cca gcc tct ccc cca gtg ggg tgg   385
Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
        115                 120                 125

aag cag agc gaa gat gcg atg cct gtt ata aat tat gat tta ctc tgt   433
Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
    130                 135                 140

gct gtt tcc aaa ttg gga cca gga gag aaa tat gaa ctt cac gcg gga   481
Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145                 150                 155                 160

aca gag tcg aca ccc agc gtg gtg gtt cat gtc tgt gaa agt gaa act   529
Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
                165                 170                 175

gaa gag gaa gaa gag aca aaa aac ccc aaa cag aaa att gcc cag aca   577
Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
            180                 185                 190

agg cgc ccc gac cct ccg acc gca gcg ttg aat gag ccc cag acc ttt   625
Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
        195                 200                 205

gat tgc gcg ctg tgaggccctt ggttgtggtg cgaggcggct gccctggtgg       677
Asp Cys Ala Leu
    210

gctctggcca tggcgctctg tgcctgcggc cgatgcgttg ctg                   720


<210> 24
<211> 212
<212> PRT
<213> Homo sapiens

<400> 24
Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
  1               5                  10                  15

Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
             20                  25                  30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
         35                  40                  45
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Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
210

<210> 25
<211> 212
<212> PRT
<213> Homo sapiens

<400> 25
Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn Glu Asp Asp
1 5 10 15

Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser Leu Phe Ala
20 25 30

Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln Lys Glu Arg
35 40 45

Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr Phe Gln Leu
50 55 60

Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys Pro Glu Ala
65 70 75 80

Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe Asn Gly Gln
85 90 95

Lys Leu Lys Leu Tyr Phe Ala Gln Ser Tyr Leu Leu Pro Pro Gln Pro
100 105 110

Val Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp
115 120 125

Lys Gln Ser Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys
130 135 140

Ala Val Ser Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly
145 150 155 160

Thr Glu Ser Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr
165 170 175

Glu Glu Glu Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr
180 185 190

Arg Arg Pro Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe
195 200 205

Asp Cys Ala Leu
210

<210> 26
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 26
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ccacagcatc ctgtttggac agcaaattcc tgagtcaagt cctgcatgct tgcaggcaga 120
cagggacaaa gtgtaagttt ctactggaaa gaggtgacgt caacacctta gtcattttcc 180
ctatgctaat taactttgct tggggagaat ggaaaaaaca gctgaggttt gctccacagc 240
atcctgtttg gacagcaaat tcctgagtca agtcctgcat gcttgcaggc agacagggac 300

aaagtgtaag tttctactgg aaagaggtga cgtcaacacc ttagtcattt tccctatgct 360
aattaacttt gcttggggag aatggaaaaa acagctgagg tttgcttcac agctgcttta 420
tcaacctctc ttgcagcata gtttccactg gtagtaattc cattcagcta ctcagacaac 480
acgctcctcg gccgaatggg acgacccttc ttaagatgga aaatgttaca aaagaaaaag 540
gatgaaggtc tgtggcaata aacagcaatt agactgtagg gaaatttcaa ggctttggga 600
aacctggaaa ccaaagtccg ggtgacatac ttgatccctg gaatttcctg aaaacctcaa 660
tcaaagtttc actttggggt attagagaaa acattttgaa atctgtcttg gtcaataaaa 720
attttaaagg acaaaaagag gaatcatttt gaagtgtagt taaaattttt ttccccagtg 780
acattttatt ggatgaatgt cccaatttct acttgtatcc cacagtggaa tggagcaaac 840
agaacctaaa acaatcctag gattttcatt tgaaaacttc attattataa tttgagaact 900
ggggatatga aacacttcga tcattttcaa agcactactg aattcaggca aaggatacaa 960
aaacactagc ctttgaaact gagcaatcta gcctttgaaa ctgagcaaag aagcattaac 1020
ccatttatgc cagaggttg 1039

<210> 27
<211> 853
<212> DNA
<213> Homo sapiens

<400> 27
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tgaaaatgat cgaagtgttt catatcccca gttctcaaat tataataatg aagttttcaa 120
atgaaaatcc taggattgtt ttaggttctg tttgctccat tccactgtgg gatacaagta 180
gaaattggga cattcatcca ataaaatgtc actggggaaa aaaattttaa ctacacttca 240
aaatgattcc tctttttgtc ctttaaaatt tttattgacc aagacagatt tcaaaatgtt 300
ttctctaata ccccaaagtg aaactttgat tgaggttttc aggaaattcc agggatcaag 360
tatgtcaccc ggactttggt ttccaggttt cccaaagtct tgaaatttcc ctacagtcta 420
attgctgttt attgccacag accttcatcc tttttctttt gtaacatttt ccatcttaag 480
aagggtcgtc ccattcggcc gaggagcgtg ttgtctgagt agctgaatgg aattactacg 540
agtggaaact atgctgcaag agaggttgat aaagcagctg tgaagcaaac ctcagctgtt 600
ttttccattc tccccaagca aagttaatta gcatagggaa aatgactaag gtgttgacgt 660
cacctctttc cagtagaaac ttacactttg tccctgtcta cctgcaagca tgcaggactt 720
gactcaggaa tttgctgtcc aaacaggatg ctgtggaagc tgcacttttt ttttccccag 780
ggagtggggg ctggccctta ctgctttata agcaccagct caagaaggaa cctacagcct 840
cttggaaagg aat 853